

10/563270

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38-21(52806)B Sequence Listing.txt  
SEQUENCE LISTING

<110> Monsanto Technology LLC

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Krasomil-Osterfeld, Karina

Pitkin, John W.

Roberts, James K.

<120> Insecticidal Proteins Secreted From Bacillus Thuringiensis and Uses Therefor

<130> 38-21(52806)B

<150> PCT/US04/21692

<151> 2004-07-06

<150> US 60/485,483

<151> 2003-07-07

<160> 33

<170> PatentIn version 3.1

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<213> Bacillus thuringiensis

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38-21(52806)B Sequence Listing.txt

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1 5

gtg gca tta tgc acc gta ccg att tta atg gtt tct aca ttc gcc agt 221
Val Ala Leu Cys Thr Val Pro Ile Leu Met Val Ser Thr Phe Ala Ser
10 15 20

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Ser Ser Met Ser Ala Phe Ala Ala Glu Ala Lys Ser Pro Asp Leu Asn
25 30 35

gta tct caa caa gta ata ggt ccc tat gcc gaa tct tat att gat att 317
Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile
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Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly
60 65 70

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Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala
75 80 85

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Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His Gln Thr Asn Arg
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Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr
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## 38-21(52806)B Sequence Listing.txt

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185 190 195	
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200 205 210 215	
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220 225 230	
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235 240 245	
cat gat tta aga aaa atg gtt tat tct ggt act cat gat cta aag ggt His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly	941
250 255 260	
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265 270 275	
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280 285 290 295	
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315 320 325	
gat act cca gct aaa ttt atg ttt aat ggt gct aat cca tat tat aga Asp Thr Pro Ala Lys Phe Met Phe Asn Gly Ala Asn Pro Tyr Tyr Arg	1181
330 335 340	
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&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Bacillus thuringiensis

&lt;400&gt; 4

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38-21(52806)B Sequence Listing.txt

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
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Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
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Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
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Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
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Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
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Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys  
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu  
275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn  
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38-21(52806)B Sequence Listing.txt

325

330

335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn  
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tttatataagg tttcatctaa ttttcaagac atgtggtgtt tttgcgtttt cttttccaa 180

atttgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact 240

gaaacatcac gatagcttaa agccaaaacga caatagtagc ggacggctac cataataata 300

tcttgtttga actgtttccc tttaaaaatat cacatttgtg attctccctcg atgctttttt 360

tagagtgttag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa 420

accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaaa catacgatgt 480

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Met Lys Tyr  
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cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct 682  
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tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca 730  
Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser

aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga 778  
Lys Ieu Thr Glv Ivs Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Glv

tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat 826  
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## 38-21(52806)B Sequence Listing.txt

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gat acc ata tat aat gga att tct gaa cta aca aat tat aca gga aca Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr Thr Gly Thr 150 155 160			1018
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38-21(52806)B Sequence Listing.txt

<212> PRT

<213> Bacillus thuringiensis

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Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp  
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Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
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Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
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Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
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Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys  
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Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
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Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Glu Thr Asn Thr  
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225 230 235 240

Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe  
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Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys  
Page 7

## 38-21(52806)B Sequence Listing.txt

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Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val  
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Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys  
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Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn  
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Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn  
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&lt;211&gt; 1552

&lt;212&gt; DNA

&lt;213&gt; Bacillus thuringiensis

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 Met Lys Tyr  
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aca att ggt act tcg agt atg tcc act ttt gct gca gaa aca aca tta 273  
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 40 45 50

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aaa cgt act ggt aaa ccg att aat atg caa gaa caa ata ata gat gga 417  
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## 38-21(52806)B Sequence Listing.txt

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38-21(52806)B Sequence Listing.txt  
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<211> 368

<212> PRT

<213> Bacillus thuringiensis

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20 25 30

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35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Ile Glu Ser Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val  
100 105 110

Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly  
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Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys  
145 150 155 160

Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val  
180 185 190

Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu  
195 200 205

38-21(52806)B Sequence Listing.txt

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr  
210 215 220

Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro  
225 230 235 240

Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys  
260 265 270

Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu  
275 280 285

Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn  
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Gly Ala Asn Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp  
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Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu  
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<212> DNA

<213> *Bacillus thuringiensis*

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tccagaaaaa acaatagtta acggagggat aata atg aaa tac aag tca tca aaa 235  
Met Lys Tyr Lys Ser Ser Lys  
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gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act 283  
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## 38-21(52806)B Sequence Listing.txt

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Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile		
40 45 50 55		
gtg cac aat aga atg aaa caa aca gat att gaa tca aaa atg aca ggt		427
Val His Asn Arg Met Lys Gln Arg Asp Ile Glu Ser Lys Met Thr Gly		
60 65 70		
aaa tcc att aat atg caa gaa caa ata att gat gga tgg ttt tta gct		475
Lys Ser Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala		
75 80 85		
aga ttt tgg ata ttt aag gat caa aat aat agt cac caa aca aat aga		523
Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Ser His Gln Thr Asn Arg		
90 95 100		
ttt att tca tgg ttt aag gat aat ttg gct agc cca gga ggg tat gat		571
Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Pro Gly Gly Tyr Asp		
105 110 115		
agt atc gct gaa cag atg ggc cta aaa gta gca gca tta aat gat atg		619
Ser Ile Ala Glu Gln Met Gly Leu Lys Val Ala Ala Leu Asn Asp Met		
120 125 130 135		
gat ata tca aat gta aat tat act tct aag aca ggg gat act ata tat		667
Asp Ile Ser Asn Val Asn Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr		
140 145 150		
aat ggt gtt tca gaa tta aaa aat atc aca gga aca act caa aaa atg		715
Asn Gly Val Ser Glu Leu Lys Asn Ile Thr Gly Thr Thr Gln Lys Met		
155 160 165		
aaa aca gat agt ttt caa aca gat tat aca aaa tcc cag tca act tca		763
Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Gln Ser Thr Ser		
170 175 180		
atc acc aat gga tta caa tta gga ttt aaa gtt tca gct aaa gga ata		811
Ile Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ser Ala Lys Gly Ile		
185 190 195		
gtg gcc tta gcc ggt gcg gat ttt gaa gca agt gta aac tat aat tta		859
Val Ala Leu Ala Gly Ala Asp Phe Glu Ala Ser Val Asn Tyr Asn Leu		
200 205 210 215		
tcc act acc gca act gaa acc aat aca ata tct gat aaa ttt acc gtt		907
Ser Thr Thr Ala Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val		
220 225 230		
cct tca caa gaa gtc aca tta gcg cca gga cat aag gcg atc gta aaa		955
Pro Ser Gln Glu Val Thr Leu Ala Pro Gly His Lys Ala Ile Val Lys		
235 240 245		
cat agt ttg aag aaa atg gta tac tct gga acg cat gat tta aaa gga		1003
His Ser Leu Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly		
250 255 260		
gat tta aca att act ttt aat gat aag gat tta gtt caa aaa ttt att		1051
Asp Leu Thr Ile Thr Phe Asn Asp Lys Asp Leu Val Gln Lys Phe Ile		
265 270 275		
tat cca aat tat aaa gct att gat tta tct aat att cgt aaa gca atg		1099
Tyr Pro Asn Tyr Lys Ala Ile Asp Leu Ser Asn Ile Arg Lys Ala Met		
280 285 290 295		
aca gaa att gat gaa tgg aat cat gta aaa cct acc gat ttc tat caa		1147
Thr Glu Ile Asp Glu Trp Asn His Val Lys Pro Thr Asp Phe Tyr Gln		
300 305 310		

38-21(52806)B Sequence Listing.txt

tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc 1195  
 Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile  
 315 320 325

gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca 1243  
 Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr  
 330 335 340

gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag 1291  
 Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys  
 345 350 355

cgt tta aat aac aaa taagttactt aaaggtaatt cattaacaat gtatccatta 1346  
 Arg Leu Asn Asn Lys  
 360

tataatataat ttataaaaat aatgttttaa aa 1378

<210> 10

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 10

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu  
 1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu  
 20 25 30

Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg  
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp  
 50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
 100 105 110

Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys  
 115 120 125

Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
 165 170 175

38-21(52806)B Sequence Listing.txt

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
275 280 285

Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn  
340 345 350

Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys  
355 360

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set forth in SEQ ID NO 3 from 438-458, biased toward codons preferred in *Bacillus* species genes containing A or T in 3rd position

<400> 11  
aataataatc atcaaacwaa t 21

<210> 12

<211> 21

38-21(52806)B Sequence Listing.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 9 78- 998, biased toward codons preferred in Bacillus species genes in which A or T is in 3rd position

<400> 12  
attwggtataw ataaatTTT g 21

<210> 13

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a B t TIC901 amino acid sequence variant

<220>

<221> CDS

<222> (1)..(1101)

<223>

<400> 13  
atg aag aac cgc ttc agc aag gtc gcc ctc tgc acg gtg cct atc ctc 48  
Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu  
1 5 10 15

atg gtt tct acg ttc gcg tcc agc tcg atg tcc gcg ttc gca gcg gag 96  
Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu  
20 25 30

gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac 144  
Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
35 40 45

gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac 192  
Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc 240  
Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac 288  
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat aac atc 336  
Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
100 105 110

gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa 384  
Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

## 38-21(52806)B Sequence Listing.txt

atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser 130 135 140	432
aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr 145 150 155 160	480
acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr 165 170 175	528
aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe 180 185 190	576
aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu 195 200 205	624
act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr 210 215 220	672
att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro 225 230 235 240	720
ggc cac aag gca atc gtc aag cac gac ctg agg aaa atg gtc tac agc Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser 245 250 255	768
ggc acc cat gat ctc aaa ggc gac ctc atc gtg tcg ttc aac gac aag Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys 260 265 270	816
gag ata gtc cag aag ttc atc tac cca aat tac cgc gac atc aac ctc Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu 275 280 285	864
agt gac atc cga gag acc atg atc gag atc gac gag tgg aac cac cgt Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val 290 295 300	912
aac cct gtc aat ttc tac gaa ctc gta gga gtt aag aac cac atc aag Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys 305 310 315 320	960
aac ggt gaa aca ttg tac atc gac acg ccg gct aag ttc atg ttc aac Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn 325 330 335	1008
gga gcg aat cct tac tat cga gct acc ttc acg gag tac gat ggc aac Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn 340 345 350	1056
aac aat cct gtt cag acc aag gtg ttg agt gag aat ttc aag ctg Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu 355 360 365	1101

&lt;210&gt; 14

&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

38-21(52806)B Sequence Listing.txt  
<223> coding sequence preferred for use in monocot species encoding a B  
t TIC901 amino acid sequence variant

<400> 14

Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu  
1 5 10 15

Met Val Ser Thr Phe Ala Ser Ser Met Ser Ala Phe Ala Ala Glu  
20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr  
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp  
50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile  
100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys  
115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr  
145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Glu Thr Thr Asn Thr  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys  
260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu  
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## 38-21(52806)B Sequence Listing.txt

275

280

285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val  
 290                   295                   300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys  
 305                   310                   315                   320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn  
 325                   330                   335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn  
 340                   345                   350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu  
 355                   360                   365

&lt;210&gt; 15

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in thermal amplification reactions

&lt;400&gt; 15

cctttggcag aaactttaac tcc

23

&lt;210&gt; 16

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in thermal amplification reactions

&lt;400&gt; 16

gtgtattctg gtacgcatga c

21

&lt;210&gt; 17

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in thermal amplification reactions

38-21(52806)B Sequence Listing.txt

mal amplification reactions

<400> 17  
gccggatccc tagctgaata tgcagtagat aatg 34

<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in thermal amplification reactions

<400> 18  
gtggcacgtt tataggccat tgttc 25

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in thermal amplification reactions

<400> 19  
cttttaggcc catctgttca gcg 23

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in thermal amplification reactions

<400> 20  
gccttagccg gtgcggattt tgaagc 26

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

38-21(52806)B Sequence Listing.txt

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in thermal amplification reactions

<400> 21 ggagcttatt tgttatcaa acgctttgtt ttgacttgat ttcc 44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

220

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in thermal amplification reactions

<400> 22  
gccggatccc agtggatagg aatttgtttt cgtgctagg 39

<210> 23

<211> 26

<212> DNA

### <213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplification of from about 600 to about 650 base pairs

<400> 23  
aayatgcarg arcarathat hgaygg 26

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24  
aayatgcarg arcarathat hga 23

<210> 25

<211> 20

38-21(52806)B Sequence Listing.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25

aayatgcarg arcarathat

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

<220>

<221> misc\_feature

<222> (3)..(3)

<223> inosine

<220>

<221> misc\_feature

<222> (9)..(9)

<223> inosine

<400> 26

ggngayacna thtayaaygg

20

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:28 and SEQ ID NO:29

38-21(52806)B Sequence Listing.txt

<220>  
<221> misc\_feature  
<222> (6)..(6)  
<223> inosine

<220>  
<221> misc\_feature  
<222> (24)..(24)  
<223> inosine

<400> 27  
tarttnggrt adatraaytt ytgnac 26

<210> 28  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:29

<220>  
<221> misc\_feature  
<222> (6)..(6)  
<223> inosine

<400> 28  
tarttnggrt adatraaytt ytg 23

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:28

<220>  
<221> misc\_feature  
<222> (18)..(18)

38-21(52806)B Sequence Listing.txt

<223> inosine

<400> 29  
ggrtadatra ayttytgnaC 20

<210> 30

<211> 570

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(570)

<223>

<400> 30  
ttt tta gct aga ttt tgg ata ttt gag gat caa aat aat aat agt cac caa 48  
Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln  
1 5 10 15

```

aca aat aga ttt att tca tgg ttt aag gat aat att gct agt tca aaa      96
Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys
          20           25           30

```

ggg tat aat agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa 144  
 Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu  
 35 40 45

aac gat atg gat gta aca aat ata gat tat aca tct aag aca ggc gat 192  
Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp  
50 55 60

acc att tat aat ggt att tca gaa ttg aaa aat tat aca gga tca act 240  
 Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr  
 65 70 75 80

caa aag atg aaa aca gat agt ttt caa aga gat tat aca aaa tca gaa      288  
 Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu  
                   85                90                95

tct act tca gta actaat gga tta caat tta gga tttaaaa gtt gct gct  
Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala  
100 105 110

aaa gga gta gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act 384  
 Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr  
     115             120             125

tat aat cta tca act act aca act gaa aca aat aca ata tca gac aag 432

130 135 140  
ttt act gtc cca tct caa gaa gtt aca ttg cct cca gga cat aaa gcg 480

145	150	155	160	
ata gtg aaa cat gat tta aga aaa atg gtt tat tct ggt act cat gat				528
Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp				

38-21(52806)B Sequence Listing.txt

cta aag ggt gat tta att gtg agt ttt aat gat aaa gag att 570  
Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile  
180 185 190

<210> 31

<211> 190

<212> PRT

<213> Bacillus thuringiensis

<400> 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln  
1 5 10 15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys  
20 25 30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu  
35 40 45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp  
50 55 60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr  
65 70 75 80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu  
85 90 95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala  
100 105 110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr  
115 120 125

Tyr Asn Leu Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys  
130 135 140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala  
145 150 155 160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp  
165 170 175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile  
180 185 190

<210> 32

<211> 1095

<212> DNA

<213> Bacillus thuringiensis

38-21(52806)B Sequence Listing.txt

<220>
 <221> CDS
 <222> (1)..(1092)
 <223> sequence encoding TIC431 precursor amino acid sequence

<400> 32
 atg aaa tac aag tct tca aaa gta gca atg tgt aca tta tcg gct tta 48  
 Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu  
 1 5 10 15

atg ctt tcg aca atc gcc act cca agt ata tct gtt ttc gct gct gaa 96  
 Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu  
 20 25 30

aca act gca tca cat aag gtt act aat cag caa aca att gca cag cgt 144  
 Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg  
 35 40 45

gca gaa tct tat atc gat att gtg cat aat aga atg aaa aaa cga gat 192  
 Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp  
 50 55 60

att gaa tca aaa atg aca ggt aaa cct att aat atg caa gaa caa ata 240  
 Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

att gat gga tgg ttt tta gct aga ttt tgg ata ttc aag gac caa aat 288  
 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

aat agt cac caa aca aat aga ttt att tca tgg ttt aaa gat aat tta 336  
 Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
 100 105 110

gct agt cca gga ggg tat aat agt atc gct aaa caa atg ggg tta aaa 384  
 Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys  
 115 120 125

ata gaa gta tta aat gat atg gat ata tca aat gta aat tat act tct 432  
 Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
 130 135 140

aag aca ggg gat act ata tat aat ggt gtt tcc gaa tta aaa aat atc 480  
 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
 145 150 155 160

aca ggt aca act caa aaa atg aaa aca gat agt ttt caa aga gat tat 528  
 Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
 165 170 175

aca aaa tca cag tca act tca atc acc aat gga tta caa tta gga ttt 576  
 Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
 180 185 190

aaa gtt tct gcc aaa ggg gtg ata gct tta gca gga gca gac ttc gaa 624  
 Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu  
 195 200 205

gca agt gtc aac tat aat tta tcc act acc gca act gaa acc aat ata 672  
 Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile  
 210 215 220

ata tct gat aaa ttt acc gtt cct tca caa gaa gtt aca tta gcg cca 720  
 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
 225 230 235 240

gga cat aag gcg atc gta aaa cat agt tta aag aaa atg gta tac tcc 768  
 Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser

## 38-21(52806)B Sequence Listing.txt

245

250

255

gga acg cat gat tta aaa gga gat tta aca att act ttt aat gat aag 816  
 Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
 260 265 270

gat tta gtt caa aaa ttt att tat cca aat tat aaa gct att gat tta 864  
 Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
 275 280 285

tct aat att cgt aaa gca ctg act gaa att gat gaa tgg aat cat gta 912  
 Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val  
 290 295 300

aaa cct acc gat ttc tat caa tta gtt ggg aac aaa aat tat ata aaa 960  
 Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
 305 310 315 320

aac ggg gac act tta tac atc gaa aca cct gct aaa ttc act ttg aat 1008  
 Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
 325 330 335

gga gga aac cct tat tat aca gca acc ttt acg gaa tat gat gaa agt 1056  
 Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser  
 340 345 350

gga aat caa gtc aaa aca aag cat tta agt gtc aaa taa 1095  
 Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys  
 355 360

&lt;210&gt; 33

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Bacillus thuringiensis

&lt;400&gt; 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu  
 1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu  
 20 25 30

Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg  
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp  
 50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile  
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn  
 85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu  
 100 105 110

Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys  
 115 120 125

38-21(52806)B Sequence Listing.txt

Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser  
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile  
145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr  
165 170 175

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe  
180 185 190

Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu  
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile  
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro  
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser  
245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys  
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu  
275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val  
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys  
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn  
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser  
340 345 350

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys  
355 360